

What is claimed is:

1. A method of genetically identifying an animal comprising:

obtaining a sample of genetic material from said animal;

5 assaying for the presence of a polymorphism in a gene selected from the group consisting of: CKM, SCN4 α , and LDH α , wherein the presence of said polymorphism is associated with favorable muscle growth and/or meat quality.

2. The method of claim 1 wherein said animal is a pig.

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3. The method of claim 1 wherein said assaying is selected from the group consisting of: restriction fragment length polymorphism (RFLP), heteroduplex analysis, single-strand conformational polymorphism (SSCP), denaturing gradient gel electrophoresis (DGGE), single base extension, mass spectrometry, oligo ligation assay (ligase chain reaction), DNA
15 sequencing and temperature gradient gel electrophoresis (TGGE).

4. The method of claim 1 further comprising amplifying an amount of said gene or a portion thereof which contains said polymorphism.

20 5. The method of claim 4 wherein said amplification includes selecting a forward a reverse primer capable of amplifying a region of said gene which contains at least one polymorphic site.

6. The method of claim 1 wherein said gene is the CKM gene.

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7. The method of claim 6 wherein said gene contains a polymorphic MspA1I site.

8. The method of claim 7 wherein said polymorphic site is amplified by primers selected from and based upon SEQ ID NO: 7 and SEQ ID NO: 8.

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9. The method of claim 6 wherein said gene contains a polymorphic BamHI site.

10. The method of claim 9 wherein said polymorphic site is amplified by primers selected from and based upon SEQ ID NO: 9 and SEQ ID NO: 10.

11. The method of claim 6 wherein said gene contains a polymorphism identified by a 9
5 base pair insertion/deletion.

12. The method of claim 11 wherein said polymorphism is amplified by primers selected from and based upon SEQ ID NO: 11 and SEQ ID NO: 12.

10 13. The method of claim 1 wherein said gene is SCN4 α .

14. The method of claim 13 wherein said gene contains a polymorphic BsrI site.

15. The method of claim 14 wherein said polymorphic site is amplified by primers
15 selected from and based upon SEQ ID NO: 13 and SEQ ID NO: 14.

16. The method of claim 13 wherein said gene contains a polymorphic PstI site.

17. The method of claim 16 wherein said polymorphic site is amplified by primers
20 selected from and based upon SEQ ID NO: 15 and SEQ ID NO: 16.

18. The method of claim 13 wherein said gene contains a polymorphic SalI site.

19. The method of claim 18 wherein said polymorphic site is amplified by primers
25 selected from and based upon SEQ ID NO: 17 and SEQ ID NO: 18.

20. The method of claim 1 wherein said gene is the LDH α gene.

21. The method of claim 20 wherein said gene contains a polymorphic AciI site.

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22. The method of claim 21 wherein said polymorphic site is amplified by a forward and a reverse primer selected from and based upon SEQ ID NO: 19 and SEQ ID NO: 20.
23. The method of claim 7 wherein said polymorphic site is a C to T single nucleotide substitution in the 5' UTR region of said gene.
24. The method of claim 9 wherein said polymorphic site is a G to T single nucleotide substitution in intron 2 of said gene.
25. The method of claim 11 wherein said 9 base pair insertion/deletion is characterized by a nucleotide sequence -TGAGCTTCC- present in allele 1 but not present in allele 2.
26. The method of claim 14 wherein said polymorphic site is a C to G single nucleotide substitution in exon 24 of said gene.
27. The method of claim 16 wherein said polymorphic site is a G to A single nucleotide substitution in exon 11 of said gene.
28. The method of claim 18 wherein said polymorphic site is a G to A single nucleotide substitution in exon 2 of said gene.
29. The method of claim 20 wherein said polymorphic site is a polymorphic base, R, wherein said base is a G or an A in exon 5 of said gene.
30. A method of screening an animal to determine said animal's genetic potential for animal breeding comprising:
obtaining a genetic sample from said animal;
identifying said animal's genotype wherein said genotype has at least one polymorphic site in a gene selected from the group consisting of: CKM, SCN4 α , and LDH α ; and
making genetic assessments based upon the presence of a polymorphism in said gene which is correlated with favorable breeding traits.

31. The method of claim 30 wherein identifying at least one polymorphic site comprises:
amplifying said sample which contains a polymorphism;
generating or destroying a restriction site in said sample;
5 determining whether a site is cleaved by a specific restriction endonuclease, wherein
cleavage of a restriction endonuclease site or an insertion or deletion indicates the
presence of a polymorphism.
32. The method of claim 31 further comprising running gel electrophoresis to identify
10 polymorphism.
33. The method of claim 30 wherein said genotype is characterized by at least one
polymorphism in the CKM gene.
- 15 34. The method of claim 33 wherein said polymorphism is identified by cleavage of a
MspAII restriction endonuclease site in a region amplified by primers SEQ ID NO: 7 and
SEQ ID NO: 8.
- 20 35. The method of claim 33 wherein said polymorphism is identified by cleavage of a
BamHI restriction endonuclease site in a region amplified by primers SEQ ID NO: 9 and
SEQ ID NO: 10.
36. The method of claim 33 wherein said polymorphism is identified by the presence or
absence of a 9 base pair insertion/deletion in a region amplified by primers SEQ ID NO:
25 11 and SEQ ID NO: 12.
37. The method of claim 30 wherein said genotype is characterized by at least one
polymorphic site in the SCN4 α gene.

38. The method of claim 37 wherein said polymorphism is identified by cleavage of a BsrI restriction endonuclease site in a region amplified by primers SEQ ID NO: 13 and SEQ ID NO: 14.

5 39. The method of claim 37 wherein said site is identified by cleavage of a PstI restriction endonuclease site in a region amplified by primers SEQ ID NO: 15 and SEQ ID NO: 16.

10 40. The method of claim 37 wherein said polymorphism is identified by cleavage of a SalI restriction endonuclease site in a region amplified by primers SEQ ID NO: 17 and SEQ ID NO: 18.

41. The method of claim 30 wherein said genotype is characterized by a polymorphism in the LDH α gene.

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42. The method of claim 41 wherein said polymorphism is identified by cleavage of an AciI restriction endonuclease site in a region amplified by primers SEQ ID NO: 19 and SEQ ID NO: 20.

20 43. The method of claim 30 wherein said animal is a pig.

44. The method of claim 30 wherein said breeding traits comprises favorable meat quality, heavy muscling, and/or skeletal muscle cramping disease.

25 45. A method of genotyping an animal to determine whether it possess a favorable combination of traits for muscle growth and/or meat quality comprising:
determining the alleles present in an animal said alleles comprising those which include one or more of the following polymorphic sites: a MspAII, BamHI, or a 9 bp insertion/deletion in a CKM gene; a BsrI, PstI, or a SalI site in a SCN4 α gene; and an AciI
30 site in a LDH α .

46. The method of claim 45 wherein said animal is a pig.

47. A method of genotyping an animal at a polymorphic locus comprising:
obtaining a genetic sample from an animal;

5 assaying for the presence of a polymorphism, said polymorphism characterized by the following:

- a) a polymorphism in the CKM gene said polymorphism located in the 5' untranslated reation of said gene (SEQ ID NO: 1);
- 10 b) a polymorphism in the CKM gene said polymorphism located in intron 2 of said gene (SEQ ID NO: 2);
- c) a polymorphism in the CKM gene said polymorphism characterized by a 9 bp insertion/deletion in intron 2 of said gene (SEQ ID NO: 2);
- d) a polymorphism in the SCN4 α gene said polymorphism located in exon 24 of said gene (SEQ ID NO: 3);
- 15 e) a polymorphism in the SCN4 α gene said polymorphism located in exon 11 of said gene (SEQ ID NO: 4);
- f) a polymorphism in the SCN4 α gene said polymorphism located in exon 2 of said gene (SEQ ID NO: 5); or
- 20 g) a polymorphism in the LDH α gene said polymorphism located in exon 5 of said gene (SEQ ID NO: 6).

48. The method of claim 47 wherein said animal is a pig.

49. A method of detecting the presence of haplotypes which is predictive for
25 determining the presence of a gene linked with favorable meat quality in an animal, said method comprising:

- a) analyzing a sample of genetic material from said animal for polymorphisms linked with meat quality traits wherein said polymorphisms are selected from the group consisting of MspA1I and a 9 bp insertion/deletion; and
- 30 b) correlating the presence of said polymorphism with the presence of said haplotypes such that said haplotypes are detected.

50. The method of claim 49 wherein said haplotypes are 1-1, 1-2 and 2-2.
51. The method of claim 49 wherein said animal is a pig.